Evaluating microbial coexistence in *in vitro* reconstructed microbial communities via stability-aware gLV identification

Matteo Turati[1], Margherita Finazzi[1], Patrizia Di Gennaro[1], Pasquale Palumbo[1]
E-mail: m.turati14@campus.unimib.it
[1] Department of Biotechnology and Biosciences, University of Milano-Bicocca, Italy

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Abstract:

Understanding whether microbial species can coexist is a central question in microbial ecology, particularly for gut microbiota studies where probiotic and dietary interventions modulate community functions. In this context, evaluating how probiotic and commensal strains interact under defined conditions requires a modelling framework capable of linking measured abundances to the resulting community behaviour.

To achieve this, we develop a stability-aware identification framework for generalized Lotka-Volterra (gLV) models that integrates stationary and time-series data with analytical feasibility and stability conditions. By enforcing these constraints during parameter identification, the inferred interaction parameters remain biologically interpretable and consistent with the expected qualitative behaviour of the community. The framework is applied to a seven-species *in vitro* reconstructed human gut microbiota comprising a four-species commensal core and a three-species probiotic consortium. Incorporating measurement noise and enforcing feasibility and stability conditions yields parameter sets that are consistent with both the data and the analytical criteria, allowing us to recover biologically meaningful pairwise interactions.

Overall, the stability-aware identification strategy provides a biologically grounded method for inferring microbial interactions and predicting coexistence across increasingly complex communities, offering a practical tool for the analysis and the design of a synthetic gut microbiota.